E. Oubns (signature)

ENTERED

#/2

RAW SEQUENCE LISTING	DATE: 08/27/2003
PATENT APPLICATION: US/09/899,422A	TIME: 12:54:43

Input Set : N:\EBONY'S\US09899422A.raw.txt
Output Set: N:\CRF4\08272003\I899422A.raw

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     1 <110> APPLICANT: Hauptmann, Rudolph
     2        Himmler, Adolph
     3        Maurer-Fogy, Ingrid
     4        Stratowa, Christian
     5 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
     6        Them
     7 <130> FILE REFERENCE: 98-385-H
C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/899,422A
     9 <141> CURRENT FILING DATE: 2001-07-03
    10 <150> PRIOR APPLICATION NUMBER: 09/525,998
    11 <151> PRIOR FILING DATE: 2000-03-15
    12 <150> PRIOR APPLICATION NUMBER: 08/383,676
    13 <151> PRIOR FILING DATE: 1995-02-01
    14 <150> PRIOR APPLICATION NUMBER: 08/153,287
    15 <151> PRIOR FILING DATE: 1993-11-17
    16 <150> PRIOR APPLICATION NUMBER: 07/821,750
    17 <151> PRIOR FILING DATE: 1992-01-02
    18 <150> PRIOR APPLICATION NUMBER: 07/511,430
    19 <151> PRIOR FILING DATE: 1990-04-20
    20 <160> NUMBER OF SEQ ID NOS: 97
    21 <170> SOFTWARE: PatentIn Ver. 2.0
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 1368
    25 <212> TYPE: DNA
    26 <213> ORGANISM: Homo sapiens
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    28 <221> NAME/KEY: CDS
    29 <222> LOCATION: (1)..(1365)
    30 <220> FEATURE:
    31 <221> NAME/KEY: sig_peptide
    32 <222> LOCATION: (1)..(87)
    33 <220> FEATURE:
    34 <221> NAME/KEY: misc_feature
    35 <222> LOCATION: (88)..(120)
    36 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
    37        extracellular proteases following secretion
    38 <220> FEATURE:
    39 <221> NAME/KEY: misc_feature
    40 <222> LOCATION: (606)..(633)
    41 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
    42        extracellular proteases following secretion
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45      Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
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47      gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct    96
48      Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
49                       20                  25                 30
50      cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa   144
51      His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
52                   35                  40                  45
53      tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa   192
54      Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
55           50                  55                  60
56      gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac   240
57      Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
58           65                  70                  75                 80
59      tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc   288
60      Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
61                       85                  90                  95
62      aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg   336
63      Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
64                   100                 105                 110
65      gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg   384
66      Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
67                   115                 120                 125
68      aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc   432
69      Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
70           130                 135                 140
71      aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag   480
72      Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
73      145                 150                 155                 160
74      aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa   528
75      Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
76                   165                 170                 175
77      aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg   576
78      Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
79                   180                 185                 190
80      aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca   624
81      Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
82                   195                 200                 205
83      ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt   672
84      Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
85                   210                 215                 220
86      tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag   720
87      Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
88      225                 230                 235                 240
89      tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag   768
90      Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
91                   245                 250                 255
92      ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc   816
93      Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
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 94                    260                 265                 270
 95        ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg    864
 96        Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
 97·                  275                 280                 285
 98        ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt    912
 99        Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
100                  290                 295                 300
101        ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg    960
102        Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
103        305                 310                 315                 320
104        gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac   1008
105        Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
106                  325                 330                 335
107        ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac   1056
108        Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
109                  340                 345                 350
110        act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg   1104
111        Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
112                  355                 360                 365
113        ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag   1152
114        Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
115        370                 375                 380
116        atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa   1200
117        Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
118        385                 390                 395                 400
119        tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc   1248
120        Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
121                  405                 410                 415
122        acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc   1296
123        Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
124                  420                 425                 430
125        tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg   1344
126        Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
127                  435                 440                 445
128        ccc gcg ccc agt ctt ctc aga tga                                   1368
129        Pro Ala Pro Ser Leu Leu Arg
130                  450                 455
132  <210> SEQ ID NO: 2
133  <211> LENGTH: 455
134  <212> TYPE: PRT
135  <213> ORGANISM: Homo sapiens
136  <400> SEQUENCE: 2
137        Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
138         1               5                  10                  15
139        Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
140                  20                 25                  30
141        His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
142              35                 40                  45
143        Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
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Input Set : **N:\EBONY'S\US09899422A.raw.txt**

Output Set: **N:\CRF4\08272003\I899422A.raw**

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144           50                    55                    60
145     Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
146     65                  70                  75                  80
147     Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
148                     85                  90                  95
149     Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
150                 100                 105                 110
151     Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
152                 115                 120                 125
153     Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
154             130                 135                 140
155     Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
156     145                 150                 155                 160
157     Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
158                 165                 170                 175
159     Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
160                 180                 185                 190
161     Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
162                 195                 200                 205
163     Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
164             210                 215                 220
165     Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
166     225                 230                 235                 240
167     Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
168                 245                 250                 255
169     Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
170                 260                 265                 270
171     Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
172                 275                 280                 285
173     Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
174             290                 295                 300
175     Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
176     305                 310                 315                 320
177     Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
178                 325                 330                 335
179     Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
180                 340                 345                 350
181     Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
182                 355                 360                 365
183     Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
184             370                 375                 380
185     Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
186     385                 390                 395                 400
187     Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
188                 405                 410                 415
189     Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
190             420                 425                 430
191     Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
192             435                 440                 445
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194            450                 455
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 483
198 <212> TYPE: DNA
199 <213> ORGANISM: Homo sapiens
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)..(483)
203 <400> SEQUENCE: 3
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206         1               5                  10                  15
207        att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt    96
208        Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
209                    20                  25                  30
210        cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc   144
211        Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
212                35                  40                  45
213        ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa   192
214        Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
215            50                  55                  60
216        tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac   240
217        Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
218        65                  70                  75                  80
219        cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg   288
220        Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
221                        85                  90                  95
222        agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg   336
223        Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
224                    100                 105                 110
225        acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc   384
226        Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
227                115                 120                 125
228        cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac   432
229        His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
230            130                 135                 140
231        tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag   480
232        Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
233        145                 150                 155                 160
234        aat                                                               483
235        Asn
237 <210> SEQ ID NO: 4
238 <211> LENGTH: 161
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 4
242        Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
243         1               5                  10                  15
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/27/2003
PATENT APPLICATION: US/09/899,422A   TIME: 12:54:44

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 344,4157,5135,6255
Seq#:28; Xaa Pos. 4
Seq#:29; Xaa Pos. 7
Seq#:32; Xaa Pos. 1,2
Seq#:36; Xaa Pos. 6,10,11,12
Seq#:41; Xaa Pos. 9,10,11
Seq#:43; Xaa Pos. 6,18
Seq#:44; Xaa Pos. 16,17
Seq#:46; Xaa Pos. 7

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/899,422A**

DATE: 08/27/2003
TIME: 12:54:44

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

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L:8 M:270 C: Current Application Number differs, Wrong Format
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:300
M:341 Repeated in SeqNo=23
L:1560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
M:341 Repeated in SeqNo=43
L:1770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
M:341 Repeated in SeqNo=44
L:1797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
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STATISTICS SUMMARY
PATENT APPLICATION: **US/09/899,422A**

DATE: 08/27/2003
TIME: 12:54:44

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

Application Serial Number: US/09/899,422A
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 07-03-2001
Art Unit: 1600
Software Application: PatentIN2.0
Total Number of Sequences: 97
Total Nucleotides: 19901
Total Amino Acids: 3746
Number of Errors: 0
Number of Warnings: 14
Number of Corrections: 1

MESSAGE SUMMARY

270 C: 1 (Current Application Number differs)
341 W: 14 ((46) "n" or "Xaa" used)